SEQUENCE LISTING

<110> Monsanto Company

<120> TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROL
      COMPOUNDS AND TOCOPHEROLS

<130> MTC 6462.1

<140> 09/548,256
<141> 2000-04-12

<150> 60/128,995
<151> 1999-04-12

<160> 31

<170> PatentIn Ver. 2.1

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<213> jojoba

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Leu Pro Val Thr Pro Gly Ser Lys Asp Lys Pro Val Val Leu Asn Ser
     50                  55                  60


Lys Lys Ser Leu Lys Glu Tyr Cys Asp Gly Asn Asn Asn Ser Leu Thr
 65                  70                  75                  80


Val Val Phe Lys Asp Leu Gly Ala Gln Val Ser Tyr Arg Thr Leu Phe
                 85                  90                  95


Phe Phe Glu Tyr Leu Gly Pro Leu Leu Ile Tyr Pro Val Phe Tyr Tyr
            100                 105                 110


Phe Pro Val Tyr Lys Phe Leu Gly Tyr Gly Glu Asp Cys Val Ile His
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Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys
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Tyr Ile Ala Tyr Tyr Val Asn His Pro Leu Tyr Thr Pro Val Ser Asp
            180   185   190

Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Leu Val Cys Gln Val Ala
            195   200   205

Asn Phe Tyr Cys His Ile Leu Leu Lys Asn Leu Arg Asp Pro Ser Gly
        210   215   220

Ala Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val Thr
225   230   235   240

Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Leu Gly Phe Asn Ile
                245   250   255

Ala Thr Gln Thr Ile Ala Gly Tyr Val Phe Leu Ala Val Ala Ala Leu
            260   265   270

Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Arg Lys Ile
        275   280   285

Phe Asp Gly Lys Asp Gly Lys Pro Lys Tyr Pro Arg Arg Trp Val Ile
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Leu Pro Pro Phe Leu
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            20                  25                  30

Ile His Ala Arg Thr Lys Lys Tyr Tyr Pro Ser Arg Gln Arg Leu Thr
            35                  40                  45

Leu Pro Leu Gln Pro Gly Lys Gly Gly Lys Pro Val Val Leu Ser Pro
        50                  55                  60

Lys Ala Ser Leu Leu Glu Tyr Cys Glu Lys Gly Ser Gly Ser Leu Thr
65                  70                  75                  80

Val Val Phe Lys Asp Leu Gly Pro Gln Val Tyr Tyr Ser Thr Leu Phe
                85                  90                  95

Phe Phe Glu Tyr Leu Gly Pro Leu Ile Ile Tyr Pro Met Phe Tyr Tyr
            100                 105                 110

Leu Pro Val Tyr Lys Tyr Phe Gly His Glu Gly Glu Arg Ala Met His
            115                 120                 125
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Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys
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Arg Ile Met Glu Thr Phe Phe Val His Arg Phe Ser Ala Thr Ser Pro
145   150   155   160

Leu Ser Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Thr Phe Gly Ala
                165   170   175

Tyr Ile Ala Tyr Tyr Cys Asn His Pro Leu Tyr Thr Pro Val Ser Asp
            180   185   190

Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Val Val Cys Gln Val Ala
            195   200   205

Asn Phe Tyr Cys His Ile Leu Leu Arg Asn Leu Arg Ser Pro Ser Gly
    210   215   220

Ser Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val Thr
225   230   235   240

Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Val Gly Phe Asn Ile
                245   250   255

Ala Thr Gln Thr Val Ala Gly Tyr Val Phe Leu Val Val Ala Ala Gly
            260   265   270

Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Lys Lys Leu
            275   280   285

Phe Asp Gly Lys Asp Gly Arg Pro Lys Tyr Pro Arg Arg Trp Val Ile
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Leu Pro Pro Phe Leu
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Ser Ala Glu Lys Gln Val Lys Leu Ser Ser Lys Ala Gly Met Leu Leu
        35   40   45

Leu Tyr Thr Pro Ala Phe Leu Ala Gly Leu Ala Ser Phe Trp Ile Phe
    50   55   60

Pro His Gln Gly Leu Arg Ser Thr Leu Leu Gln Ser Ala Val Thr Leu
65   70   75   80

His Phe Phe Lys Arg Val Phe Glu Val Val Phe Ile His Lys Tyr Ser
                85   90   95

Gly Ala Met Leu Leu Asp Ser Ala Ile Pro Ile Thr Leu Ser Tyr Phe
            100   105   110

Leu Ser Thr Ala Thr Met Ile Tyr Ala Gln His Leu Thr Gln Gly Leu
        115   120   125

Pro Glu Pro Pro Ile Asp Leu Leu Tyr Pro Gly Ile Val Leu Phe Val
        130   135   140

Val Gly Ile Ile Gly Asn Phe Tyr His His Tyr Leu Leu Ser Asn Leu
145   150   155   160

6

Arg Gly Lys Gly Glu Lys Glu Tyr Lys Ile Pro Lys Gly Gly Met Phe
            165   170   175

Glu Leu Val Ile Cys Pro His Tyr Leu Phe Glu Ile Ile Glu Phe Tyr
            180   185   190

Gly Phe Ser Phe Ile Ser Gln Thr Leu Tyr Ala Phe Ser Phe Thr Val
         195   200   205

Gly Thr Thr Leu Tyr Leu Leu Gly Arg Ser Tyr Ser Thr Arg Lys Trp
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Tyr Leu Ser Lys Phe Glu Asp Phe Pro Glu His Val Lys Ala Ile Ile
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Pro Phe Val Phe

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Asn Ala Phe Leu Ser Glu Ile Arg Gly Lys His Leu Asn Tyr Ser Lys
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Phe Trp Asn Ala Asn Pro Ser Ala Glu Lys Gln Val Lys Leu Ser Ser
    50   55   60

Lys Ala Gly Met Leu Leu Leu Tyr Thr Pro Ala Phe Leu Ala Gly Leu
65   70   75   80

Ala Ser Phe Trp Val Phe Pro His Gln Gly Leu Arg Phe Thr Ile Leu
                85   90   95

Gln Ser Ala Val Thr Leu His Tyr Phe Lys Arg Val Phe Glu Gly Leu
        100   105   110

Phe Ile His Lys Tyr Ser Gly Gly Met Thr Leu Glu Ser Ala Ile Pro
    115   120   125

Ile Thr Leu Ser Tyr Phe Leu Ser Ala Val Thr Met Val Tyr Ser Gln
    130   135   140

His Leu Thr Lys Gly Phe Pro Glu Pro Pro Ile Asn Leu Phe Tyr Pro
145   150   155   160

Gly Ile Val Leu Phe Leu Val Gly Ile Ile Gly Asn Phe Tyr His His
            165   170   175

Tyr Leu Leu Ser Lys Leu Arg Gly Lys Gly Glu Lys Glu Tyr Lys Ile
        180   185   190

Pro Lys Gly Gly Phe Phe Glu Leu Val Ile Cys Pro His Tyr Phe Phe
    195   200   205

Glu Ile Thr Val Phe Tyr Gly Ile Phe Phe Ile Ser Gln Thr Leu Tyr
    210   215   220

Ser Phe Ala Phe Ala Val Gly Thr Thr Met Tyr Leu Val Gly Arg Ser
225   230   235   240

Tyr Ser Thr Arg Lys Trp Tyr Leu Ser Lys Phe Glu Asp Phe Pro Lys

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Ser Asp Ser Ser Asn Gly Leu Leu Leu Ser Gly Ser Asp Asn Asn Ser
            35                  40                  45

Pro Ser Asp Asp Val Gly Ala Pro Ala Asp Val Arg Asp Arg Ile Asp
        50                  55                  60

Ser Val Val Asn Asp Asp Ala Gln Gly Thr Ala Asn Leu Ala Gly Asp
65                  70                  75                  80

Asn Asn Gly Gly Gly Asp Asn Asn Gly Gly Gly Arg Gly Gly Gly Glu
                85                  90                  95

Gly Arg Gly Asn Ala Asp Ala Thr Phe Thr Tyr Arg Pro Ser Val Pro
                100                 105                 110

Ala His Arg Arg Ala Arg Glu Ser Pro Leu Ser Ser Asp Ala Ile Phe
            115                 120                 125

Lys Gln Ser His Ala Gly Leu Phe Asn Leu Cys Val Val Val Leu Ile
        130                 135                 140

Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly Trp
145                 150                 155                 160

Leu Ile Arg Thr Asp Phe Trp Phe Ser Ser Arg Ser Leu Arg Asp Trp
                165                 170                 175

Pro Leu Phe Met Cys Cys Ile Ser Leu Ser Ile Phe Pro Leu Ala Ala
                180                 185                 190

Phe Thr Val Glu Lys Leu Val Leu Gln Lys Tyr Ile Ser Glu Pro Val
            195                 200                 205

Val Ile Phe Leu His Ile Ile Ile Thr Met Thr Glu Val Leu Tyr Pro
        210                 215                 220

Val Tyr Val Thr Leu Arg Cys Asp Ser Ala Phe Leu Ser Gly Val Thr
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10

Leu Met Leu Leu Thr Cys Ile Val Trp Leu Lys Leu Val Ser Tyr Ala
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His Thr Ser Tyr Asp Ile Arg Ser Leu Ala Asn Ala Ala Asp Lys Ala
                260   265   270

Asn Pro Glu Val Ser Tyr Tyr Val Ser Leu Lys Ser Leu Ala Tyr Phe
        275   280   285

Met Val Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Ser Ala
    290   295   300

Cys Ile Arg Lys Gly Trp Val Ala Arg Gln Phe Ala Lys Leu Val Ile
305   310   315   320

Phe Thr Gly Phe Met Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro Ile
                325   330   335

Val Arg Asn Ser Lys His Pro Leu Lys Gly Asp Leu Leu Tyr Ala Ile
                340   345   350

Glu Arg Val Leu Lys Leu Ser Val Pro Asn Leu Tyr Val Trp Leu Cys
        355   360   365

Met Phe Tyr Cys Phe Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu
    370   375   380

Leu Cys Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys
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Ser Val Gly Asp Tyr Trp Arg Met Trp Asn Met Pro Val His Lys Trp
                405   410   415

Met Val Arg His Ile Tyr Phe Pro Cys Leu Arg Ser Lys Ile Pro Lys
                420   425   430

Thr Leu Ala Ile Ile Ile Ala Phe Leu Val Ser Ala Val Phe His Glu
        435   440   445

Leu Cys Ile Ala Val Pro Cys Arg Leu Phe Lys Leu Trp Ala Phe Leu
    450   455   460

Gly Ile Met Phe Gln Val Pro Leu Val Phe Ile Thr Asn Tyr Leu Gln
465   470   475   480

Glu Arg Phe Gly Ser Thr Val Gly Asn Met Ile Phe Trp Phe Ile Phe

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<210> 14
<211> 496
<212> PRT
<213> Caenorhabditis elegans

<400> 14

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Asn Gly Ser Leu Ala Ser Ser Arg Arg Ser Ser Phe Ala Gln Asn Gly
               20   25   30

Asn Ser Ser Arg Lys Ser Ser Glu Met Arg Gly Pro Cys Glu Lys Val
          35   40   45

Val His Thr Ala Gln Asp Ser Leu Phe Ser Thr Ser Ser Gly Trp Thr
     50   55   60

Asn Phe Arg Gly Phe Phe Asn Leu Ser Ile Leu Leu Leu Val Leu Ser
 65   70   75   80

Asn Gly Arg Val Ala Leu Glu Asn Val Ile Lys Tyr Gly Ile Leu Ile
               85   90   95

Thr Pro Leu Gln Trp Ile Ser Thr Phe Val Glu His His Tyr Ser Ile
          100   105   110

Trp Ser Trp Pro Asn Leu Ala Leu Ile Leu Cys Ser Asn Ile Gln Ile
          115   120   125

Leu Ser Val Phe Gly Met Glu Lys Ile Leu Glu Arg Gly Trp Leu Gly
     130   135   140

Asn Gly Phe Ala Ala Val Phe Tyr Thr Ser Leu Val Ile Ala His Leu
145   150   155   160

Thr Ile Pro Val Val Val Thr Leu Thr His Lys Trp Lys Asn Pro Leu
               165   170   175

Trp Ser Val Val Met Met Gly Val Tyr Val Ile Glu Ala Leu Lys Phe
          180   185   190

Ile Ser Tyr Gly His Val Asn Tyr Trp Ala Arg Asp Ala Arg Arg Lys
          195   200   205

Ile Thr Glu Leu Lys Thr Gln Val Thr Asp Leu Ala Lys Lys Thr Cys
     210   215   220

Asp Pro Lys Gln Phe Trp Asp Leu Lys Asp Glu Leu Ser Met His Gln
225   230   235   240

Met Ala Ala Gln Tyr Pro Ala Asn Leu Thr Leu Ser Asn Ile Tyr Tyr
          245   250   255

13

Phe Met Ala Ala Pro Thr Leu Cys Tyr Glu Phe Lys Phe Pro Arg Leu
        260   265   270

Leu Arg Ile Arg Lys His Phe Leu Ile Lys Arg Thr Val Glu Leu Ile
        275   280   285

Phe Leu Ser Phe Leu Ile Ala Ala Leu Val Gln Gln Trp Val Val Pro
        290   295   300

Thr Val Arg Asn Ser Met Lys Pro Leu Ser Glu Met Glu Tyr Ser Arg
305   310   315   320

Cys Leu Glu Arg Leu Leu Lys Leu Ala Ile Pro Asn His Leu Ile Trp
            325   330   335

Leu Leu Phe Phe Tyr Thr Phe Phe His Ser Phe Leu Asn Leu Ile Ala
            340   345   350

Glu Leu Leu Arg Phe Ala Asp Arg Glu Phe Tyr Arg Asp Phe Trp Asn
        355   360   365

Ala Glu Thr Ile Gly Tyr Phe Trp Lys Ser Trp Asn Ile Pro Val His
        370   375   380

Arg Phe Ala Val Arg His Ile Tyr Ser Pro Met Met Arg Asn Asn Phe
385   390   395   400

Ser Lys Met Ser Ala Phe Phe Val Val Phe Phe Val Ser Ala Phe Phe
            405   410   415

His Glu Tyr Leu Val Ser Val Pro Leu Lys Ile Phe Arg Leu Trp Ser
            420   425   430

Tyr Tyr Gly Met Met Gly Gln Ile Pro Leu Ser Ile Ile Thr Asp Lys
            435   440   445

Val Val Arg Gly Gly Arg Thr Gly Asn Ile Ile Val Trp Leu Ser Leu
        450   455   460

Ile Val Gly Gln Pro Leu Ala Ile Leu Met Tyr Gly His Asp Trp Tyr
465   470   475   480

Ile Leu Asn Phe Gly Val Ser Ala Val Gln Asn Gln Thr Val Gly Ile
            485   490   495

14

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<211> 257
<212> DNA
<213> Glycine max

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cctcttgggg gatctaagaa aaagctacta aatgtgtggg ttgttttcac atttgttgca 180
atctggcatg atttagagtg gaagcttctt tcatgggcat ggttgacgtg tttattcttc 240
atccctgagt tggtttt 257

<210> 16
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<212> DNA
<213> Glycine max

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<223> n=a, t, c or g

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atatttacag gagttatggg atttataata gaacaataca ttaatcccat tgtacaaaat 180
tcacagcatc ctctcaaggg aaaccttctt tacgccatcg agagagttct gaag 234

<210> 17
<211> 275
<212> DNA
<213> Glycine max

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15

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<222> (244)..(245)
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<222> (251)
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gatgatccgc cacctatatt ttccatgttt aaggcacggt ataccaaagg ccgttgctct  120
tttaattgcc ttcctggttc tgctttattc catgagctgt gcatcgctgt tccttgccca  180
catattcaag tngtgggttt cngnggaatt nagtttcagg tnccttgggt ttcnaccnna  240
attnntnggc naaaaaattc cnngaacccc ggggg                              275
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<210> 18
<211> 267
<212> DNA
<213> Glycine max

<400> 18

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tgtcatatgc acatacaaac tatgatatga gagcacttac tgtttcgaat gaaaagggag  120
aaacattacc caatactttg atatggagta tccgtacact gtgaccttca ggagtttggc  180
atacttcatg gttgctccta cattatgcta tcagacaagc tatcctcgca caccttcagt  240
tcgaaagggt tgggtgtttc gtcaact                                       267
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<210> 19
<211> 1895
<212> DNA
<213> Human

<220>
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<223> n=a, t, c or g

<400> 19

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ggctgccgcc ctgagctcgg gctgggacgt gcccagaggt gttgggagga tctggggtga  180
gtaccctgtg gccaggacta aaggggctnc accctcctgt ccatccctcg cagatcttga  240
gcaatgcccg gttatttctg gagaacctca tcaagtatgg catcctggtg gaccccatcc  300
aggtggtttc tctgttcctg aaggatccct atagctggcc cgccccatgc ctggttattg  360
cggccaatgt ctttgctgtg gctgcattcc aggttgagaa gcgcctggcg gtgggtgccc  420
tgacggagca ggcgggactg ctgctgcacg tggccaacct ggccaccatt ctgtgtttcc  480
cagcggctgt ggtcttactg gttgagtcta tcactccagt gggctccctg ctggcgctga  540
tggcgcacac catcctcttc ctcaagctct ctcctaccg cgacgtcaac tcatggtgcc  600
gcagggccag ggccaaggct gcctctgcag ggaagaaggc cagcagtgct gctgccccgc  660
acaccgtgag ctacccggac aatctgacct accgcgatct ctactacttc ctcttcgccc  720
ccaccttgtg ctacgagctc aactttcccc gctctccccg catccggaag cgctttctgc  780
tgcgacggat ccttgagatg ctgttcttca cccagctcca ggtggggctg atccagcagt  840
ggatggtccc caccatccag aactccatga gcccttcaa ggacatggac tactcacgca  900
tcatcgagcg cctcctgaag ctggcggtcc ccaatcacct catctggctc atcttcttct  960
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17

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tccctgtgca caagtggtgc atcagacact tctacaagcc catgcttcga cggggcagca 1140
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tgagcgtccc tctgcgaatg ttccgcctct gggcgttcac gggcatgatg gctcagatcc 1260
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gggcgggcat ggccggtagg gggagtgcaa ggccaggcag acgcccccat tccccacact 1860
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<210> 20
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<212> DNA
<213> Montierella alphina

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<222> (22)
<223> n=a, t, c or g

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<223> n=a, t, c or g

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aacggagcac tatatttacc ccgtggtngt tcaacccagc catctcaccc ttgcgagcat 180
tggtgctgct cttgataccc ttcatgctta actatctcat gatcttttac atcattttcg 240
agtgcatctg caacgccttt gcggaactaa gttgctttgc ggatcgcaac ttttacgagg 300
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acttcttgct ccgccacgtg tacgactcga gcatccgagt ccttccactt gtccgaaatc 420
caatgccgcn aattgcaaac gttccttccc ggtcgtcaat gcgttcaacg aacctgggtg 480
aagaatgggt ggtgacaacg ttaaagtgcg cccggtatc 519

<210> 21
<211> 518
<212> DNA
<213> mouse

<400> 21
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gtcaacctgt ggtgccgcca gcgaagggtc aaggccaaag ctgtctctac agggaagaag 180
gtcagtgggg ctgctgcgag caagctgtga gctatccaga caacctgacc taccgagatc 240
tcgattactt catctttgct cctactttgt gttatgaact caactttcct cggtccccccc 300
gaatacgaga gcgctttctg ctacgacgag ttcttgagat gctctttttt acccagcttc 360
aagtggggct gatccaacag tggatggtcc ctactatcca gaactccatg gaagcccttt 420
caagagcttc tgcagttttg gagaccgcga gttctacaga gattggtgga atgctgagtc 480
tgtcaccgac ttttggcaga actggaatat ccccgtgg 518

<210> 22
<211> 299
<212> DNA
<213> mouse

<400> 22
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gcaatgcagc tgtgtgggtg acactcatca ttgggcaacc ggtggctgtc tcatgtatgt 120
ccacgactac tacgtgctca actacgatgc cccagtgggt catgagctac tgccaaaggc 180
agccctccct aacctgggcc tggagttctg gaggggttcc tggctgcctg cacactcctc 240
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<212> DNA
<213> Rat

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tagacgaaga ggaggtgcga gacgccgctg tgggccccga cttgggcgcc gggggtgacg 180
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<212> PRT
<213> rat

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            20   25   30

Glu Val Arg Asp Ala Ala Val Gly Pro Asp Leu Gly Ala Gly Gly Asp
            35   40   45

Ala Pro Ala Pro Ala Pro Val Pro Ala Pro Ala His Thr Arg Asp Lys
        50   55   60

Asp Arg Gln Thr Ser Val Gly Asp Gly His Trp Glu Leu Arg Cys His
65   70   75   80

Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr
            85   90   95

Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala
            100   105   110

Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro
            115   120   125

Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala
    130   135   140

Pro Cys Leu Ile Ile Ala Ser Asn Ile Phe Ile Val Ala Thr Phe Gln
145   150   155   160

Ile Glu Lys Arg Leu Ser Val Gly Ala Leu Thr Glu Gln Met Gly Leu
            165   170   175

Leu Leu His Val Val Asn Leu Ala Thr Ile Ile Cys Phe Pro Ala Ala
            180   185   190

Val Ala Leu Leu Val Glu Ser Ile Thr Pro Val Gly Ser Leu Phe Ala
            195   200   205

Leu Ala Ser Tyr Ser Ile Ile Phe Leu Lys Leu Phe Ser Tyr Arg Asp
    210   215   220

Val Asn Leu Trp Cys Arg Gln Arg Arg Val Lys Ala Lys Ala Val Ser
225   230   235   240

Ala Gly Lys Lys Val Ser Gly Ala Ala Ala Gln Asn Thr Val Ser Tyr
            245   250   255

Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Ile Phe Ala Pro
            260   265   270

22

Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys
        275   280   285

Arg Phe Leu Leu Arg Arg Val Leu Glu Met Leu Phe Phe Thr Gln Leu
    290   295   300

Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile Gln Asn Ser
305   310   315   320

Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu
                325   330   335

Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr
            340   345   350

Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Leu Gln Phe
        355   360   365

Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ala Glu Ser Val Thr
    370   375   380

Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg
385   390   395   400

His Phe Tyr Lys Pro Met Leu Arg Leu Gly Ser Asn Lys Trp Met Ala
                405   410   415

Arg Thr Gly Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val
            420   425   430

Ser Ile Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met
        435   440   445

Ala Gln Val Pro Leu Ala Trp Ile Val Asn Arg Phe Phe Gln Gly Asn
    450   455   460

Tyr Gly Asn Ala Ala Val Trp Val Thr Leu Ile Ile Gly Gln Pro Val
465   470   475   480

Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Asp Ala
                485   490   495

Pro Val Gly Ala
        500

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23

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aagatatctc catgctacgt tcaagcatgt aatggtgggc aacatgatan tttggntctn   180
cagtatagtc ggacagccga tgtnnnnnna tctatactac catgacgtca tgaacaggca   240
ggcccaggca agtagatagt ncggcagaga catgtacttc aacatcganc atcagnagca   300
nacngagcga gcggcangaa ncagc   325

<210> 26
<211> 262
<212> DNA
<213> Zea mays

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aaagttggca ttcaacaatc tcattagtga tcctgctact acctgttttc acatcctttt   180
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26

<210> 27
<211> 253
<212> DNA
<213> Zea mays

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atgagttatg tgttgctgtt ccctgccaca tactcaagtt ctgggctttt tttaggaatc 180
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atggttggca ata   253

<210> 28
<211> 254
<212> DNA
<213> Zea mays

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aaaagttggc attcaacaat ctcattagtg atcctgctac tacctgtttt cacatccttt 180
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<212> DNA
<213> Maize

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27

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<211> 541
<212> PRT
<213> Maize


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<223> Xaa=any amino acid

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                20   25   30

Met Asp Asn Cys Lys Pro Cys Gly Gly Ala Ile Pro Leu Cys Met Val
            35   40   45

Ser Glu Phe Asp Leu Pro Leu Asp Leu Val Asp Arg Lys Val Arg Lys
        50   55   60

Met Lys Met Ile Ser Pro Ser Asn Val Ala Val Asp Ile Gly Arg Thr
65   70   75   80

Leu Ala Pro His Glu Tyr Ile Gly Met Val Arg Arg Glu Val Leu Asp
                85   90   95

Ala Tyr Leu Arg Ser Arg Ala Gln Ser Val Gly Ala Glu Val Val Asn
            100   105   110

Gly Leu Phe Leu Arg Tyr Glu Ala Pro Lys Glu Pro Asn Gly Ser Tyr
        115   120   125

Val Val His Tyr Asn His Tyr Asp Gly Ser Asn Gly Lys Val Gly Gly
    130   135   140

Glu Lys Arg Ser Phe Glu Val Asp Ala Ile Val Gly Ala Asp Gly Ala
145   150   155   160

Asn Ser Arg Val Ala Asn Asp Met Gly Ala Gly Asp Tyr Glu Tyr Ala
                165   170   175

Ile Ala Phe Gln Glu Arg Val Lys Ile Pro Asp Asp Lys Met Val Tyr
            180   185   190

Tyr Glu Glu Arg Ala Glu Met Tyr Val Gly Asp Asp Val Ser Pro Asp
        195   200   205

Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp His Val Ala Val Gly Thr

29

Gly Thr Val Thr His Lys Ala Asp Ile Lys Lys Phe Gln Ala Ala Thr
225   230   235   240

Arg Leu Arg Ala Lys Asp Lys Ile Glu Gly Gly Lys Ile Ile Arg Val
                245   250   255

Glu Ala His Pro Ile Pro Glu His Pro Arg Pro Lys Arg Val Ser Gly
            260   265   270

Arg Val Thr Leu Val Gly Asp Ala Ala Gly Tyr Val Thr Lys Cys Ser
            275   280   285

Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser Gly Arg Met Cys Ala Glu
        290   295   300

Ala Ile Val Ala Gly Ser Ala Asn Gly Thr Arg Met Val Glu Glu Ser
305   310   315   320

Asp Leu Arg Lys Tyr Leu Ala Glu Phe Asp Arg Leu Tyr Trp Pro Thr
            325   330   335

Tyr Lys Val Leu Asp Ile Leu Gln Lys Val Phe Tyr Arg Ser Asn Ala
            340   345   350

Ala Arg Glu Ala Phe Val Glu Met Cys Ala Asp Asp Tyr Val Gln Lys
            355   360   365

Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg Val Val Pro Gly Asn Pro
    370   375   380

Leu Asp Asp Ile Lys Leu Ala Val Asn Thr Ile Gly Ser Leu Val Arg
385   390   395   400

Ala Thr Ala Leu Arg Arg Glu Met Glu Lys Val Thr Leu Xaa Ala Ala
            405   410   415

Ala Arg Asp Val Ile Ala Val Glu Met Val Ser Gln Leu Ile Gly Arg
            420   425   430

Cys Ile Ser Arg Asp Leu Arg Leu Ile Gly Leu Ile Xaa Ala Asn Met
            435   440   445

Arg Gly Gln Trp Ala Arg Arg Gly Arg Glu Thr Ser Cys Ala Ser Ala
    450   455   460

Ala Ser Arg Ser Lys Val Leu Pro Val Cys Ile Asp Gly Ser Cys Asn

Ile Xaa His Leu Val Met Leu Arg Ile Arg Ser Ser Ser Ser Thr Gly
              485   490   495

Phe Xaa Arg Arg Gln Ala Ser Thr Ser Met Asn Val Xaa Tyr Leu Val
          500   505   510

His Gln Asp Met Xaa Xaa Asn Xaa Asn Ser Pro Val Leu Val Gln Lys
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Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Gly Arg
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<212> PRT
<213> Artificial Sequence

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Ala Gly Ala Gly Met Val Ala Pro Phe Thr Gly Leu Lys Ser Met Ala
              20   25   30

Gly Phe Pro Phe Thr Gly Leu Lys Ser Met Ala Gly Phe Pro Thr Arg
          35   40   45

Lys Thr Asn Asn Asp Ile Thr Ser Ile Ala Ser Asn Gly Gly Arg Val
    50   55   60

Gln Cys Met Gln Val Trp Pro Pro Ile Gly Lys Lys Lys Phe Glu Thr
 65   70   75   80